



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/709,572	05/14/2004	Itzhak Bentwich	050992.0202.01USCP	3571
37808	7590	10/29/2007		
ROSETTA-GENOMICS c/o PSWS 700 W. 47TH STREET SUITE 1000 KANSAS CITY, MO 64112			EXAMINER WOLLENBERGER, LOUIS V	
			ART UNIT 1635	PAPER NUMBER
			MAIL DATE 10/29/2007	DELIVERY MODE PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice to Comply	Application No.	Applicant(s)	
	10709572	BENTWICH ET AL.	
	Examiner	Art Unit	
	Louis V. Wollenberger	1635	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set in the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: The sequence listings submitted on 1/30/2007 could not be accepted due to errors. See the attached Validation Report.

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the specification.**
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-2510

For CRF Submission Help, call (571) 272-2501/2583.

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Notice to Comply with Sequence Rules

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth below or on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

In the instant case, the sequence listings submitted on 1/30/2007 could not be accepted due to errors. See the attached Validation Report.

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Louis V. Wollenberger whose telephone number is 571-272-8144. The examiner can normally be reached on M-F, 8 am to 4:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James Schultz can be reached on (571)272-0763. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Art Unit: 1635

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

LW

October 24, 2007

/Sean McGarry/
Primary Examiner
AU 1635

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Mark Spencer

Timestamp: Wed May 16 16:15:29 EDT 2007

=====

Reviewer Comments:

E254 The total number of bases conflicts with running total, Input: 22, Calculated : 17 SEQID
(6710511)

E253 The number of bases differs from <211> Input: 12 Calculated:17 SEQID (6710511)

<210> 6710511

<211> 12

<212> DNA

<213> Homo sapiens

<400> 6710511

catatacctc tt

<211> 22

<212> DNA

<213> Homo sapiens

<400> 6710519

catatagcat tgataatctt ca

22

Fix – Change the number of bases to the right of sequence for 6710511 to 12.

Missing SEQ ID # 6710512 to complete SEQ ID # 6710519.

E254 The total number of bases conflicts with running total, Input: 22, Calculated : 24 SEQID
(9319192)

E253 The number of bases differs from <211> Input: 22 Calculated:24 SEQID (9319192)

<210> 9319192

<211> 22

<212> DNA

<213> Homo sapiens

<400> 9319192

aatgaaatga agatatgatc ag

1> 22

<212> DNA

<213> Homo sapiens

<400> 9319201

aatgcagtga gccattaaat gg

2

Fix – Change the number of bases to the right of sequence for 9319192 to 22.

Missing SEQ ID # 9319193 to complete SEQ ID # 9319201.

E202 Invalid input format; Value must be an integer in <210> in SEQID (9974642)

E249 Order Sequence Error <210> -> <213>; Expected Mandatory Tag: <211> in SEQID (9974642)

<210> 9974642

<211> 22

<212> DNA

<213> Homo sapiens

<400> 9974642

tctcagggct cagagctcag gc 22

<210> 9972> DNA

<213> Homo sapiens

<400> 9974651

tctcctgccca ctgcttccca tt 22

Fix – Missing SEQ ID # 9974643 to complete SEQ ID # 9974651.

E254 The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID (10068324)

E253 The number of bases differs from <211> Input: 18 Calculated:20 SEQID (10068324)

This is OK no fix is required.

E252 Calc# of Seq. differs from actual; 10068324 seqIds defined; count=10068237

Fix – Numeric Identifier <160> says there is a total of 10068324 sequences. The computer only counted 10068237.

Provide the missing sequences above or adjust the numbering of the sequences and change <160> to reflect the actual total.

Application No: 10709572

Version No: 1.0

Started: 2007-04-26 15:09:46.706

Finished: 2007-04-26 18:23:53.100

Elapsed: 3 hr(s) 14 min(s) 6 sec(s) 394 ms

Total Warnings: 0

Total Errors: 75

No. of SeqIDs Defined: 10068324

Actual SeqID Count: 10068237

ErrCode	Error Description
E 212	Invalid Sequence ID Number; Expected 165602 as next SeqID but skipped to 165603
E 212	Invalid Sequence ID Number; Expected 329702 as next SeqID but skipped to 329703
E 212	Invalid Sequence ID Number; Expected 493802 as next SeqID but skipped to 493803
E 212	Invalid Sequence ID Number; Expected 657902 as next SeqID but skipped to 657903
E 212	Invalid Sequence ID Number; Expected 822002 as next SeqID but skipped to 822003
E 212	Invalid Sequence ID Number; Expected 986102 as next SeqID but skipped to 986103
E 212	Invalid Sequence ID Number; Expected 1148302 as next SeqID but skipped to 1148303
E 212	Invalid Sequence ID Number; Expected 1310302 as next SeqID but skipped to 1310303
E 212	Invalid Sequence ID Number; Expected 1472302 as next SeqID but skipped to 1472303
E 212	Invalid Sequence ID Number; Expected 1634302 as next SeqID but skipped to 1634303
E 212	Invalid Sequence ID Number; Expected 1796302 as next SeqID but skipped to 1796303
E 212	Invalid Sequence ID Number; Expected 1958302 as next SeqID but skipped to 1958303
E 212	Invalid Sequence ID Number; Expected 2120302 as next SeqID but skipped to 2120303
E 212	Invalid Sequence ID Number; Expected 2282302 as next SeqID but skipped to 2282303

Started: 2007-04-26 15:09:46.706
Finished: 2007-04-26 18:23:53.100
Elapsed: 3 hr(s) 14 min(s) 6 sec(s) 394 ms
Total Warnings: 0
Total Errors: 75
No. of SeqIDs Defined: 10068324
Actual SeqID Count: 10068237

ErrCode	Error Description
E 212	Invalid Sequence ID Number; Expected 2444302 as next SeqID but skipped to 2444303
E 212	Invalid Sequence ID Number; Expected 2606302 as next SeqID but skipped to 2606303
E 212	Invalid Sequence ID Number; Expected 2768302 as next SeqID but skipped to 2768303
E 212	Invalid Sequence ID Number; Expected 2930302 as next SeqID but skipped to 2930303
E 212	Invalid Sequence ID Number; Expected 3092302 as next SeqID but skipped to 3092303
E 212	Invalid Sequence ID Number; Expected 3254302 as next SeqID but skipped to 3254303 This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total, Input: 22, Calculated : 17 SEQID(6710511)
E 253	The number of bases differs from <211> Input: 12 Calculated:17 SEQID (6710511)
E 254	The total number of bases conflicts with running total, Input: 22, Calculated : 24 SEQID(9319192)
E 253	The number of bases differs from <211> Input: 22 Calculated:24 SEQID (9319192)
E 202	Invalid input format; Value must be an integer in <210> in SEQID (9974642)
E 249	Order Sequence Error <210> -> <213>; Expected Mandatory Tag: <211> in SEQID (9974642)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(10068324)
E 253	The number of bases differs from <211> Input: 18 Calculated:20 SEQID (10068324)
E 252	Calc# of Seq. differs from actual; 10068324 seqIds defined; count=10068237
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> ROSETTA GENOMICS LTD

Bentwich, Itzhak

Avniel, Amir

<120> BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
OLIGONUCLEOTIDES AND USES THEREOF

<130> 050992.0202.CPUS01

<140> 10/709,572

<141> 2004-05-14

<160> 10068324

<170> PatentIn version 3.3

<210> 1

<211> 17

<212> DNA

<213> Homo sapiens

<400> 1

gcgcctgtgc ctcttaa 17

<210> 2

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2

gctcccactg ctgtcctgcc at 22

<210> 3

<211> 22

<212> DNA

<213> Homo sapiens

<400> 3

gctgcacttc agcctgggtg tc 22

<210> 4

<211> 22

<212> DNA

<213> Homo sapiens

<400> 4

gctggctcca cctgctgcca gg 22

<210> 5

<211> 21

<212> DNA

<213> Homo sapiens

<400> 5

ggaatggtgg ttgtatggtt g 21

<210> 6

<211> 23

<212> DNA

<213> Homo sapiens

<400> 6

ggccaagtgg atgctggttt agc 23

<210> 7

<211> 22

<212> DNA

<213> Homo sapiens

<400> 7

ggccgggtgc tctggaggtg ct 22

<210> 8

<211> 22

<212> DNA

<213> Homo sapiens

<400> 8
ggccgtggtc gctgactctc gt 22

<210> 9
<211> 22
<212> DNA
<213> Homo sapiens

<400> 9
ggctgggtag atttggtg gc tt 22

<210> 10
<211> 22
<212> DNA
<213> Homo sapiens

<400> 10
gggaaataat taatgtgaag tc 22

<210> 11
<211> 22
<212> DNA
<213> Homo sapiens

<400> 11
ggggaacgcg ctggcccgcg cc 22

<210> 12
<211> 19
<212> DNA
<213> Homo sapiens

<400> 12
gggtctctgt tggcttctt 19

<210> 13
<211> 22

<212> DNA
<213> Homo sapiens

<400> 13
gggttactct gtgttggtca gg 22

<210> 14
<211> 22
<212> DNA
<213> Homo sapiens

<400> 14
ggtggcccct gggagatgct gg 22

<210> 15
<211> 22
<212> DNA
<213> Homo sapiens

<400> 15
gtcagtcatt gaatgctggc ct 22

<210> 16
<211> 22
<212> DNA
<213> Homo sapiens

<400> 16
gtgcggcctg gccttcaagt gg 22

<210> 17
<211> 22
<212> DNA
<213> Homo sapiens

<400> 17
gtgcttaaag aatggctgtc cg 22

<210> 18
<211> 19
<212> DNA
<213> Homo sapiens

<400> 18
gtttctctgg gcttggcat 19

<210> 19
<211> 20
<212> DNA
<213> Homo sapiens

<400> 19
tagcatggct ctatggaaca 20

<210> 20
<211> 22
<212> DNA
<213> Homo sapiens

<400> 20
taggtatggc ttgtggcaca gc 22

<210> 21
<211> 22
<212> DNA
<213> Homo sapiens

<400> 21
tattcattgc ccatgtttgt ga 22

<210> 22
<211> 22
<212> DNA
<213> Homo sapiens

<400> 22
tcaactgcaac ctccaccttc ag 22

<210> 23
<211> 22
<212> DNA
<213> Homo sapiens

<400> 23
tccagctgtc cacgtcttcc tg 22

<210> 24
<211> 23
<212> DNA
<213> Homo sapiens

<400> 24
tccaggccct caatccattt cca 23

<210> 25
<211> 22
<212> DNA
<213> Homo sapiens

<400> 25
tcccagctcc tgggccccac ag 22

<210> 26
<211> 22
<212> DNA
<213> Homo sapiens

<400> 26
tccttcctct gtcaggcagg cc 22

<210> 27
<211> 22
<212> DNA
<213> Homo sapiens